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        RAW SEQUENCE LISTING              DATE: 11/06/2000
        PATENT APPLICATION:  US/09/348,815    TIME: 11:22:56

        Input Set : A:\126p1d1-sl.txt
        Output Set: N:\CRF3\11062000\I348815.raw

        SEQUENCE LISTING
     4 (1) GENERAL INFORMATION:
     6      (i) APPLICANT: LI, HAODONG
     7                     ADAMS, MARK D
     9     (ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR-2
    11    (iii) NUMBER OF SEQUENCES: 6
    13     (iv) CORRESPONDENCE ADDRESS:
    14          (A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.
    15          (B) STREET: 9410 KEY WEST AVENUE
    16          (C) CITY: ROCKVILLE
    17          (D) STATE: MD
    18          (E) COUNTRY: US
    19          (F) ZIP: 20850
    21      (v) COMPUTER READABLE FORM:
    22          (A) MEDIUM TYPE: Floppy disk
    23          (B) COMPUTER: IBM PC compatible
    24          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    25          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
    27     (vi) CURRENT APPLICATION DATA:
C--> 28          (A) APPLICATION NUMBER: US/09/348,815
C--> 29          (B) FILING DATE: 08-Jul-1999
    30          (C) CLASSIFICATION:
    32   (viii) ATTORNEY/AGENT INFORMATION:
    33          (A) NAME: JONATHAN L. KLEIN
    34          (B) REGISTRATION NUMBER: 41,119
    35          (C) REFERENCE/DOCKET NUMBER: PF126P1D1
    37     (ix) TELECOMMUNICATION INFORMATION:
    38          (A) TELEPHONE: 301-309-8504
    39          (B) TELEFAX: 301-309-8439
    42 (2) INFORMATION FOR SEQ ID NO: 1:
    44      (i) SEQUENCE CHARACTERISTICS:
    45          (A) LENGTH: 1146 base pairs
    46          (B) TYPE: nucleic acid
    47          (C) STRANDEDNESS: single
    48         ·(D) TOPOLOGY: linear
    50     (ii) MOLECULE TYPE: DNA (genomic)
    53     (ix) FEATURE:
    54          (A) NAME/KEY: CDS
    55          (B) LOCATION: 1..1146
    58     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
    60 ATG AGC TCC CGC ATC GCC AGG GCG CTC GCC TTA GTC GTC ACC CTT CTC    48
    61 Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu Leu
    62  1               5                  10                  15
    64 CAC TTG ACC AGG CTG GCG CTC TCC ACC TGC CCC GCT GCC TGC CAC TGC    96
    65 His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
    66             20                  25                  30
    68 CCC CTG GAG GCG CCC AAG TGC GCG CCG GGA GTC GGG CTG GTC CGG GAC   144
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 69 Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
 70         35              40              45
 72 GGC TGC GGC TGC TGT AAG GTC TGC GCC AAG CAG CTC AAC GAG GAC TGC   192
 73 Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
 74     50              55              60
 76 AGC AAA ACG CAG CCC TGC GAC CAC ACC AAG GGG CTG GAA TGC AAC TTC   240
 77 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
 78 65              70              75              80
 80 GGC GCC AGC TCC ACC GCT CTG AAG GGG ATC TGC AGA GCT CAG TCA GAG   288
 81 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
 82              85              90              95
 84 GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA AGT   336
 85 Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
 86          100             105             110
 88 TTC CAG CCC AAC TGT AAA CAT CAG TGC ACA TGT ATT GAT GGC GCC GTG   384
 89 Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
 90          115             120             125
 92 GGC TGC ATT CCT CTG TGT CCC CAA GAA CTA TCT CTC CCC AAC TTG GGC   432
 93 Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
 94      130             135             140
 96 TGT CCC AAC CCT CGG CTG GTC AAA GTT ACC GGG CAG TGC TGC GAG GAG   480
 97 Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu
 98 145             150             155             160
100 TGG GTC TGT GAC GAG GAT AGT ATC AAG GAC CCC ATG GAG GAC CAG GAC   528
101 Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp
102              165             170             175
104 GGC CTC CTT GGC AAG GAG CTG GGA TTC GAT GCC TCC GAG GTG GAG TTG   576
105 Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu Leu
106          180             185             190
108 ACG AGA AAC AAT GAA TTG ATT GCA GTT GGA AAA GGC AGC TCA CTG AAG   624
109 Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Ser Ser Leu Lys
110          195             200             205
112 CGG CTC CCT GTT TTT GGA ATG GAG CCT CGC ATC CTA TAC AAC CCT TTA   672
113 Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu
114      210             215             220
116 CAA GGC CAG AAA TGT ATT GTT CAA ACA ACT TCA TGG TCC CAG TGC TCA   720
117 Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser
118 225             230             235             240
120 AAG ACC TGT GGA ACT GGT ATC TCC ACA CGA GTT ACC AAT GAC AAC CCT   768
121 Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro
122              245             250             255
124 GAG TGC CGC CTT GTG AAA GAA ACC CGG ATT TGT GAG GTG CGG CCT TGT   816
125 Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys
126          260             265             270
128 GGA CAG CCA GTG TAC AGC AGC CTG AAA AAG GGC AAG AAA TGC AGC AAG   864
129 Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys
130          275             280             285
132 ACC AAG AAA TCC CCC GAA CCA GTC AGG TTT ACT TAC GCT GGA TGT TTG   912
133 Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu
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                    Input Set : A:\126p1d1-sl.txt
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134      290                    295                    300
136 AGT GTG AAG AAA TAC CGG CCC AAG TAC TGC GGT TCC TGC GTG GAC GGC    960
137 Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly
138 305                    310                    315                    320
140 CGA TGC TGC ACG CCC CAG CTG ACC AGG ACT GTG AAG ATG CGG TTC CGC   1008
141 Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg
142                    325                    330                    335
144 TGC GAA GAT GGG GAG ACA TTT TCC AAG AAC GTC ATG ATG ATC CAG TCC   1056
145 Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln Ser
146                    340                    345                    350
148 TGC AAA TGC AAC TAC AAC TGC CCG CAT GCC AAT GAA GCA GCG TTT CCC   1104
149 Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe Pro
150      355                    360                    365
152 TTC TAC AGG CTG TTC AAT GAC ATT CAC AAA TTT AGG GAC TAA           1146
153 Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp
154      370                    375                    380
157 (2) INFORMATION FOR SEQ ID NO: 2:
159      (i) SEQUENCE CHARACTERISTICS:
160           (A) LENGTH: 381 amino acids
161           (B) TYPE: amino acid
162           (D) TOPOLOGY: linear
164      (ii) MOLECULE TYPE: protein
166      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
168 Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu Leu
169  1                5                    10                    15
170 His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
171           20                    25                    30
172 Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
173           35                    40                    45
174 Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
175      50                    55                    60
176 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
177 65                    70                    75                    80
178 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
179           85                    90                    95
180 Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
181           100                    105                    110
182 Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
183           115                    120                    125
184 Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
185      130                    135                    140
186 Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu
187 145                    150                    155                    160
188 Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp
189           165                    170                    175
190 Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu Leu
191           180                    185                    190
192 Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Ser Ser Leu Lys
193           195                    200                    205
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RAW SEQUENCE LISTING   DATE: 11/06/2000
PATENT APPLICATION: US/09/348,815   TIME: 11:22:56

Input Set : A:\126pld1-sl.txt
Output Set: N:\CRF3\11062000\I348815.raw

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194 Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu
195     210             215             220
196 Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser
197 225             230             235             240
198 Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro
199     245             250             255
200 Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys
201     260             265             270
202 Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys
203     275             280             285
204 Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu
205     290             295             300
206 Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly
207 305             310             315             320
208 Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg
209     325             330             335
210 Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln Ser
211     340             345             350
212 Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe Pro
213     355             360             365
214 Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp
215     370             375             380
219 (2) INFORMATION FOR SEQ ID NO: 3:
221     (i) SEQUENCE CHARACTERISTICS:
222         (A) LENGTH: 28 base pairs
223         (B) TYPE: nucleic acid
224         (C) STRANDEDNESS: single
225         (D) TOPOLOGY: linear
227     (ii) MOLECULE TYPE: DNA (genomic)
230     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
232 CGCGGGATCC TGCGCGACAC AATGAGCT                              28
234 (2) INFORMATION FOR SEQ ID NO: 4:
236     (i) SEQUENCE CHARACTERISTICS:
237         (A) LENGTH: 30 base pairs
238         (B) TYPE: nucleic acid
239         (C) STRANDEDNESS: single
240         (D) TOPOLOGY: linear
242     (ii) MOLECULE TYPE: DNA (genomic)
245     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
247 CGCGGGTACC AGGTAGCATT TAGTCCCTAA                            30
249 (2) INFORMATION FOR SEQ ID NO: 5:
251     (i) SEQUENCE CHARACTERISTICS:
252         (A) LENGTH: 27 base pairs
253         (B) TYPE: nucleic acid
254         (C) STRANDEDNESS: single
255         (D) TOPOLOGY: linear
257     (ii) MOLECULE TYPE: DNA (genomic)
260     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
262 AAAGGATCCA CAATGAGCTC CCGAATC                               27
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RAW SEQUENCE LISTING   DATE: 11/06/2000
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  Input Set : A:\126p1d1-sl.txt
  Output Set: N:\CRF3\11062000\I348815.raw

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264 (2) INFORMATION FOR SEQ ID NO: 6:
266      (i) SEQUENCE CHARACTERISTICS:
267          (A) LENGTH: 58 base pairs
268          (B) TYPE: nucleic acid
269          (C) STRANDEDNESS: single
270          (D) TOPOLOGY: linear
272     (ii) MOLECULE TYPE: DNA (genomic)
275     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
277 CGCTCTAGAT TAAGCGTAGT CTGGGACGTC GTATGGGTAT TGGAACAGCC TGTAGAAG        58
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VERIFICATION SUMMARY   DATE: 11/06/2000
PATENT APPLICATION: US/09/348,815   TIME: 11:22:57

Input Set : A:\126pld1-sl.txt
Output Set: N:\CRF3\11062000\I348815.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]